



SEQUENCE LISTING

<110> Structural GenomiX, Inc.
Atwell, Shane
Buchanan, Sean G.

<120> Crystals and Structures of Epidermal Growth Factor Receptor Kinase Domain

<130> 022132-000910US

<140> 10/801,266

<141> 2004-03-16

<150> US 60/456,553

<151> 2003-03-20

<160> 8

<170> PatentIn version 3.1

<210> 1

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> forward primer

<400> 1

gtcccaacc aagctctc

18

<210> 2

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> reverse primer

<400> 2

cccctgaat gacaaggtag

20

<210> 3
 <211> 26
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> sequence after being ligated into vector

<400> 3
 aaggcatca tcaccatcac cactga 26

<210> 4
 <211> 297
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> predicted sequence of EGFRKD expressed protein

<400> 4

Met Ala Leu Ala Pro Asn Gln Ala Leu Leu Arg Ile Leu Lys Glu Thr
 1 5 10 15

Glu Phe Lys Lys Ile Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val
 20 25 30

Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu Lys Val Lys Ile Pro Val
 35 40 45

Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser Pro Lys Ala Asn Lys Glu
 50 55 60

Ile Leu Asp Glu Ala Tyr Val Met Ala Ser Val Asp Asn Pro His Val
 65 70 75 80

Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Ile Thr
 85 90 95

Gln Leu Met Pro Phe Gly Cys Leu Leu Asp Tyr Val Arg Glu His Lys
 100 105 110

Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn Trp Cys Val Gln Ile Ala
 115 120 125

Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg Leu Val His Arg Asp Leu
130 135 140

Ala Ala Arg Asn Val Leu Val Lys Thr Pro Gln His Val Lys Ile Thr
145 150 155 160

Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala Glu Glu Lys Glu Tyr His
165 170 175

Ala Glu Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile
180 185 190

Leu His Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val
195 200 205

Thr Val Trp Glu Leu Met Thr Phe Gly Ser Lys Pro Tyr Asp Gly Ile
210 215 220

Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu Lys Gly Glu Arg Leu Pro
225 230 235 240

Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys
245 250 255

Trp Met Ile Asp Ala Asp Ser Arg Pro Lys Phe Arg Glu Leu Ile Ile
260 265 270

Glu Phe Ser Lys Met Ala Arg Asp Pro Gln Arg Tyr Leu Val Ile Gln
275 280 285

Gly Glu Gly His His His His His His
290 295

<210> 5

<211> 290

<212> PRT

<213> Homo sapiens

<400> 5

Met Ala Leu Ala Pro Asn Gln Ala Leu Leu Arg Ile Leu Lys Glu Thr
1 5 10 15

Glu Phe Lys Lys Ile Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val

20	25	30
Tyr Lys Gly Leu Trp Ile Pro Glu Gly Glu Lys Val Lys Ile Pro Val		
35	40	45
Ala Ile Lys Glu Leu Arg Glu Ala Thr Ser Pro Lys Ala Asn Lys Glu		
50	55	60
Ile Leu Asp Glu Ala Tyr Val Met Ala Ser Val Asp Asn Pro His Val		
65	70	75
80		
Cys Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Ile Thr		
85	90	95
Gln Leu Met Pro Phe Gly Cys Leu Leu Asp Tyr Val Arg Glu His Lys		
100	105	110
Asp Asn Ile Gly Ser Gln Tyr Leu Leu Asn Trp Cys Val Gln Ile Ala		
115	120	125
Lys Gly Met Asn Tyr Leu Glu Asp Arg Arg Leu Val His Arg Asp Leu		
130	135	140
Ala Ala Arg Asn Val Leu Val Lys Thr Pro Gln His Val Lys Ile Thr		
145	150	155
160		
Asp Phe Gly Leu Ala Lys Leu Leu Gly Ala Glu Glu Lys Glu Tyr His		
165	170	175
Ala Glu Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile		
180	185	190
Leu His Arg Ile Tyr Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val		
195	200	205
Thr Val Trp Glu Leu Met Thr Phe Gly Ser Lys Pro Tyr Asp Gly Ile		
210	215	220
Pro Ala Ser Glu Ile Ser Ser Ile Leu Glu Lys Gly Glu Arg Leu Pro		
225	230	235
240		
Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys		
245	250	255
Trp Met Ile Asp Ala Asp Ser Arg Pro Lys Phe Arg Glu Leu Ile Ile		
260	265	270

Glu Phe Ser Lys Met Ala Arg Asp Pro Gln Arg Tyr Leu Val Ile Gln
275 280 285

Gly Glu
290

<210> 6

<211> 289

<212> PRT

<213> Unknown

<220>

<223> HER2/ErbB2

<400> 6

Ser Gly Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr
1 5 10 15

Glu Leu Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val
20 25 30

Tyr Lys Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val
35 40 45

Ala Ile Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu
50 55 60

Ile Leu Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val
65 70 75 80

Ser Arg Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr
85 90 95

Gln Leu Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg
100 105 110

Gly Arg Leu Gly Ser Gln Asp Leu Leu Asn Trp Cys Met Gln Ile Ala
115 120 125

Lys Gly Met Ser Tyr Leu Glu Asp Val Arg Leu Val His Arg Asp Leu
130 135 140

Ala Ala Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr

145 150 155 160
 Asp Phe Gly Leu Ala Arg Leu Leu Asp Ile Asp Glu Thr Glu Tyr His
 165 170 175
 Ala Asp Gly Gly Lys Val Pro Ile Lys Trp Met Ala Leu Glu Ser Ile
 180 185 190
 Leu Arg Arg Arg Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val
 195 200 205
 Thr Val Trp Glu Leu Met Thr Phe Gly Ala Lys Pro Tyr Asp Gly Ile
 210 215 220
 Pro Ala Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro
 225 230 235 240
 Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Ile Met Val Lys Cys
 245 250 255
 Trp Met Ile Asp Ser Glu Cys Arg Pro Arg Phe Arg Glu Leu Val Ser
 260 265 270
 Glu Phe Ser Arg Met Ala Arg Asp Pro Gln Arg Phe Val Val Ile Gln
 275 280 285

Asn

<210> 7
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 <212> PRT
 <213> Unknown

 <220>
 <223> HER4/ErbB4

 <400> 7

Ser Gly Thr Ala Pro Asn Gln Ala Gln Leu Arg Ile Leu Lys Glu Thr
 1 5 10 15
 Glu Leu Lys Arg Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val
 20 25 30

Tyr Lys Gly Ile Trp Val Pro Glu Gly Glu Thr Val Lys Ile Pro Val
35 40 45

Ala Ile Lys Ile Leu Asn Glu Thr Thr Gly Pro Lys Ala Asn Val Glu
50 55 60

Phe Met Asp Glu Ala Leu Ile Met Ala Ser Met Asp His Pro His Leu
65 70 75 80

Val Arg Leu Leu Gly Val Cys Leu Ser Pro Thr Ile Gln Leu Val Thr
85 90 95

Gln Leu Met Pro His Gly Cys Leu Leu Glu Tyr Val His Glu His Lys
100 105 110

Asp Asn Ile Gly Ser Gln Leu Leu Leu Asn Trp Cys Val Gln Ile Ala
115 120 125

Lys Gly Met Met Tyr Leu Glu Glu Arg Arg Leu Val His Arg Asp Leu
130 135 140

Ala Ala Arg Asn Val Leu Val Lys Ser Pro Asn His Val Lys Ile Thr
145 150 155 160

Asp Phe Gly Leu Ala Arg Leu Leu Glu Gly Asp Glu Lys Glu Tyr Asn
165 170 175

Ala Asp Gly Gly Lys Met Pro Ile Lys Trp Met Ala Leu Glu Cys Ile
180 185 190

His Tyr Arg Lys Phe Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val
195 200 205

Thr Ile Trp Glu Leu Met Thr Phe Gly Gly Lys Pro Tyr Asp Gly Ile
210 215 220

Pro Thr Arg Glu Ile Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Pro
225 230 235 240

Gln Pro Pro Ile Cys Thr Ile Asp Val Tyr Met Val Met Val Lys Cys
245 250 255

Trp Met Ile Asp Ala Asp Ser Arg Pro Lys Phe Lys Glu Leu Ala Ala
260 265 270

Glu Phe Ser Arg Met Ala Arg Asp Pro Gln Arg Tyr Leu Val Ile Gln

275	280	285
Gly Asp		
290		
<210> 8		
<211> 289		
<212> PRT		
<213> Unknown		
<220>		
<223> HER3/ErbB3		
<400> 8		
Ser Glu Lys Ala Asn Lys Val Leu Ala Arg Ile Phe Lys Glu Thr Glu		
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Leu Arg Lys Leu Lys Val Leu Gly Ser Gly Val Phe Gly Thr Val His		
20	25	30
Lys Gly Val Trp Ile Pro Glu Gly Glu Ser Ile Lys Ile Pro Val Cys		
35	40	45
Ile Lys Val Ile Glu Asp Lys Ser Gly Arg Gln Ser Phe Gln Ala Val		
50	55	60
Thr Asp His Met Leu Ala Ile Gly Ser Leu Asp His Ala His Ile Val		
65	70	75 80
Arg Leu Leu Gly Leu Cys Pro Gly Ser Ser Leu Gln Leu Val Thr Gln		
85	90	95
Tyr Leu Pro Leu Gly Ser Leu Leu Asp His Val Arg Gln His Arg Gly		
100	105	110
Ala Leu Gly Pro Gln Leu Leu Leu Asn Trp Gly Val Gln Ile Ala Lys		
115	120	125
Gly Met Tyr Tyr Leu Glu Glu His Gly Met Val His Arg Asn Leu Ala		
130	135	140
Ala Arg Asn Val Leu Leu Lys Ser Pro Ser Gln Val Gln Val Ala Asp		
145	150	155 160

Phe Gly Val Ala Asp Leu Leu Pro Pro Asp Asp Lys Gln Leu Leu Tyr
165 170 175

Ser Glu Ala Lys Thr Pro Ile Lys Trp Met Ala Leu Glu Ser Ile His
180 185 190

Phe Gly Lys Tyr Thr His Gln Ser Asp Val Trp Ser Tyr Gly Val Thr
195 200 205

Val Trp Glu Leu Met Thr Phe Gly Ala Glu Pro Tyr Ala Gly Leu Arg
210 215 220

Leu Ala Glu Val Pro Asp Leu Leu Glu Lys Gly Glu Arg Leu Ala Gln
225 230 235 240

Pro Gln Ile Cys Thr Ile Asp Val Tyr Met Val Met Val Lys Cys Trp
245 250 255

Met Ile Asp Glu Asn Ile Arg Pro Thr Phe Lys Glu Leu Ala Asn Glu
260 265 270

Phe Thr Arg Met Ala Arg Asp Pro Pro Arg Tyr Leu Val Ile Lys Arg
275 280 285

Glu

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